Sequence Listing

<110> ASHKENAZI, AVI J
BOTSTEIN, DAVID
DODGE, KELLY H.
GURNEY, AUSTIN L.
KIM, KYUNG JIN
LAWRENCE, DAVID A.
PITTI, ROBERT
ROY, MARGARET A
TUMAS, DANIEL B
WOOD, WILLIAM I.

<120> DcR3 Polypeptide, A TNFR Homolog

<130> P1134R2 REVISED

<140> US 09/157,289
<141> 1998-09-18

<150> US 60/059,288
<151> 1997-09-18

<150> US 60/094,640
<151> 1998-07-30

<160> 18

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<212> PRT
<213> Homo sapiens

<400> 1

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Leu Ala Leu Pro Ala Leu Leu Pro Val Pro Ala Val Arg Gly Val
            20                  25                  30

Ala Glu Thr Pro Thr Tyr Pro Trp Arg Asp Ala Glu Thr Gly Glu
            35                  40                  45

Arg Leu Val Cys Ala Gln Cys Pro Pro Gly Thr Phe Val Gln Arg
            50                  55                  60

Pro Cys Arg Arg Asp Ser Pro Thr Thr Cys Gly Pro Cys Pro Pro
            65                  70                  75

Arg His Tyr Thr Gln Phe Trp Asn Tyr Leu Glu Arg Cys Arg Tyr
            80                  85                  90
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Cys Asn Val Leu Cys Gly Glu Arg Glu Glu Glu Ala Arg Ala Cys
95 100 105

His Ala Thr His Asn Arg Ala Cys Arg Cys Arg Thr Gly Phe Phe
110 115 120

Ala His Ala Gly Phe Cys Leu Glu His Ala Ser Cys Pro Pro Gly
125 130 135

Ala Gly Val Ile Ala Pro Gly Thr Pro Ser Gln Asn Thr Gln Cys
140 145 150

Gln Pro Cys Pro Pro Gly Thr Phe Ser Ala Ser Ser Ser Ser Ser
155 160 165

Glu Gln Cys Gln Pro His Arg Asn Cys Thr Ala Leu Gly Leu Ala
170 175 180

Leu Asn Val Pro Gly Ser Ser Ser His Asp Thr Leu Cys Thr Ser
185 190 195

Cys Thr Gly Phe Pro Leu Ser Thr Arg Val Pro Gly Ala Glu Glu
200 205 210

Cys Glu Arg Ala Val Ile Asp Phe Val Ala Phe Gln Asp Ile Ser
215 220 225

Ile Lys Arg Leu Gln Arg Leu Leu Gln Ala Leu Glu Ala Pro Glu
230 235 240

Gly Trp Gly Pro Thr Pro Arg Ala Gly Arg Ala Ala Leu Gln Leu
245 250 255

Lys Leu Arg Arg Arg Leu Thr Glu Leu Leu Gly Ala Gln Asp Gly
260 265 270

Ala Leu Leu Val Arg Leu Leu Gln Ala Leu Arg Val Ala Arg Met
275 280 285

Pro Gly Leu Glu Arg Ser Val Arg Glu Arg Phe Leu Pro Val His
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<211> 1114
<212> DNA
<213> Homo sapiens

<220>
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agggtcctgt gtccgcgctg agccgcgctc tccctgctcc agcaaggacc 100

atgagggcgc tggaggggcc aggcctgtcg ctgctgtgcc tggtgttggc 150

gctgcctgcc ctgctgccgg tgccggctgt acgcggagtg gcagaaacac 200

ccacctaccc ctggcgggac gcagagacag gggagcggct ggtgtgcgcc 250

cagtgccccc caggcacctt tgtgcagcgg ccgtgccgcc gagacagccc 300

cacgacgtgt ggcccgtgtc caccgcgcca ctacacgcag ttctggaact 350

acctggagcg ctgccgctac tgcaacgtcc tctgcgggga gcgtgaggag 400

gaggcacggg cttgccacgc cacccacaac cgtgcctgcc gctgccgcac 450

cggcttcttc gcgcacgctg gtttctgctt ggagcacgca tcgtgtccac 500

ctggtgccgg cgtgattgcc ccgggcaccc ccagccagaa cacgcagtgc 550

cagccgtgcc ccccaggcac cttctcagcc agcagctcca gctcagagca 600

gtgccagccc caccgcaact gcacggccct gggcctggcc ctcaatgtgc 650

caggctcttc ctcccatgac accctgtgca ccagctgcac tggcttcccc 700

ctcagcacca gggtaccagg agctgaggag tgtgagcgtg ccgtcatcga 750

ctttgtggct ttccaggaca tctccatcaa gaggctgcag cggctgctgc 800

aggccctcga ggccccggag ggctggggtc cgacaccaag ggcgggccgc 850

gcggccttgc agctgaagct gcgtcggcgg ctcacggagc tcctgggggc 900

gcaggacggg gcgctgctgg tgcggctgct gcaggcgctg cgcgtggcca 950

ggatgcccgg gctggagcgg agcgtccgtg agcgcttcct ccctgtgcac 1000

tgatcctggc cccctcttat ttattctaca tccttggcac cccacttgca 1050

ctgaaagagg ctttttttta aatagaagaa atgaggtttn ttaaaaaaaa 1100

aaaaaaaaaa aaaa 1114

<210> 3
<211> 491

<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<220>
<221> unsure
<222> 62, 73, 86, 98
<223> unknown base

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cagttctgga antaactgga gcnctgccgc tactgnaacg tcctctgngg 100

ggagcgtgag gaggaggcac gggcttgcca cgccacccac aaccgtgcct 150

gccgctgccg caccggcttc ttcgcgcacg ctggtttctg cttggagcac 200

gcatcgtgtc cacctggtgc cggcgtgatt gccccgggca cccccagcca 250

gaacacgcag tgcctagccg tgcccccccag gcaccttctc agccagcagc 300

tccagctcag agcagtgcca gccccaccgc aactgcacgg ccctgggcct 350

ggccctcaat gtgccaggct cttcctccca tgacaccctg tgcaccagct 400

gcactggctt ccccctcagc accagggtac caggagctga ggagtgtgag 450

cgtgccgtca tcgactttgt ggctttccag gacatctcca t 491

<210> 4
<211> 73
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

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gccgagacag ccccacgacg tgtggcccgt gtccaccgcg ccactacacg 50

cattctggaa ctacctggag cgc 73

<210> 5
<211> 271
<212> DNA
<213> Unknown

<220>

<223> Unknown organism

<220>
<221> unsure
<222> 42, 62, 73, 86, 98, 106, 120, 122, 153, 167, 184, 220, 233
<223> unknown base

<400> 5
gccgagacag ccccacgacg tgtggcccgt gtccaccgcg cnactacacg 50

cagttctgga antaactgga gcnctgccgc tactgnaacg tcctctgngg 100

ggagcntgag gaggaggcan gngcttgcca cgccacccac aaccgcgcct 150

gcngctgcag caccggnttc ttcgcgcacg ctgntttctg cttggagcac 200

gcatcgtgtc cacctggtgn cggcgtgatt gcnccgggca cccccagcca 250

gaacacgcat gcaaagccgt g 271

<210> 6
<211> 201
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<220>
<221> unsure
<222> 182
<223> unknown base

<400> 6
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gggagcgtga ggaggaggca cgggcttgcc acgccaccca caaccgtgcc 100

tgccgctgcc gcaccggctt cttcgcgcac gctggtttct gcttggagca 150

cgcatcgtgt ccacctggtg ccggcgtgat tnccccgggc acccccagcc 200

a 201

<210> 7
<211> 277
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<220>
<221> unsure
<222> 142
<223> unknown base

<400> 7
gaggggcccc caggagtggt ggccggaggt gtggcagggg tcaggttgct 50

ggtcccagcc ttgcaccctg agctaggaca ccagttcccc tgaccctgtt 100

cttccctcct ggctgcaggc acccccagcc agaacacgca gnccagccgt 150

gccccccagg caccttctca gccagcagct ccagctcaga gcagtgccag 200

ccccaccgca actgcacggc cctgggcctg gccctcaatg tgccaggctc 250

ttcctcccat gacaccctgt gcaccag 277

<210> 8
<211> 199
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<400> 8
gcatcgtgtc cacctggtgc cggcgtgatt gccccgggca cccccagcca 50

gaacacgcag gcctagccgt gccccccagg caccttctca gccagcagct 100

ccagctcaga gcagtgccag ccccaccgca actgcacggc cctgggcctg 150

gccctcaatg tgccaggctc ttcctcccat gacaccctgt gcaccagct 199

<210> 9
<211> 226
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<220>
<221> unsure
<222> 4, 9, 12, 165
<223> unknown base

<400> 9
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tgccagcccc accgcaactg cacggccctg ggcctggccc tcaatgtgcc 100

aggctcttcc tcccatgaca cgctgtgcac cagctgcact ggcttccccc 150

tcagcaccag ggtancagga gctgaggagt gtgagcgtgc cgtcatcgac 200

tttgtggctt tccaggacat ctccat 226

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<211> 283
<212> DNA
<213> Homo sapiens

<220>
<221> Unsure
<222> 1-283
<223> Unknown organism

<220>
<221> unsure
<222> 27, 64, 140
<223> unknown base

<400> 10
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cgcagtgcca gccntccccc caggcacctt ctcagccagc agctccagct 100

cagagcagtg ccagccccac cgcaactgca acgccctggn ctggccctca 150

atgtgccagg ctcttcctcc catgacaccc tgtgcaccag ctgcactggc 200

ttccccctca gcaccagggt accaggagct gaggagtgtg agcgtgccgt 250

catcgacttt gtggctttcc aggacatctc cat 283

<210> 11
<211> 21
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<400> 11
cacgctggtt tctgcttgga g 21

<210> 12
<211> 22
<212> DNA

<213> Unknown

<220>
<223> Unknown organism

<400> 12
agctggtgca cagggtgtca tg 22

<210> 13
<211> 53
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<400> 13
cccaggcacc ttctcagcca gccagcagct ccagctcaga gcagtgccag 50

ccc 53

<210> 14
<211> 24
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<400> 14
acacgatgcg tgctccaagc agaa 24

<210> 15
<211> 17
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<400> 15
cttcttcgcg cacgctg 17

<210> 16
<211> 16
<212> DNA
<213> Unknown

<220>
<223> Unknown organism

<400> 16
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<210> 17
<211> 461
<212> PRT
<213> Homo sapiens

<400> 17

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Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu
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Leu Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr
             20                  25                  30

Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr
             35                  40                  45

Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly
             50                  55                  60

Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys
             65                  70                  75

Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val
             80                  85                  90

Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val
             95                 100                 105

Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys
            110                 115                 120

Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg
            125                 130                 135

Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
            140                 145                 150

Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala
            155                 160                 165

Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg
            170                 175                 180

Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser
            185                 190                 195

Arg Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala
            200                 205                 210
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Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln
215 220 225

His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
230 235 240

Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr
245 250 255

Gly Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala
260 265 270

Leu Gly Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr
275 280 285

Gln Val Lys Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val
290 295 300

Pro His Leu Pro Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu
305 310 315

Gln Gln His Leu Leu Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser
320 325 330

Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg Arg Ala Pro Thr Arg
335 340 345

Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly Glu
350 355 360

Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His
365 370 375

Gly Thr Gln Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser
380 385 390

Ser Asp His Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met
395 400 405

Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln
410 415 420

Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu
425 430 435

Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro
440 445 450

Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser
455 460

<210> 18
<211> 293
<212> PRT
<213> Homo sapiens

<400> 18

Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser
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Ile Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His
20 25 30

Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro
35 40 45

Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr
50 55 60

Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His
65 70 75

Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu
80 85 90

Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys
95 100 105

Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys
110 115 120

His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr
125 130 135

Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe
140 145 150

Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn
155 160 165

Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr
170 175 180

His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys
185 190 195

Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala
200 205 210

Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp
215 220 225

Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile
230 235 240

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys
245 250 255

Leu Trp Lys His Gln Asn Lys Ala Gln Asp Ile Val Lys Lys Ile
260 265 270

Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile
275 280 285

Gly His Ala Asn Leu Thr Phe Glu
290